RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10

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IFW16

RAW SEQUENCE LISTING DATE: 02/04/2005
PATENT APPLICATION: US/10/644,123A TIME: 07:26:30

Input Set : D:\UF-314XC1.txt

```
3 <110 > APPLICANT: Richards, Nigel Gordon John
              Chang, Christopher Harry
              Peck, Ammon B.
      7 <120> TITLE OF INVENTION: Polunucleotides Encoding Oxalate Decarboxylase from
Aspergillus
     8
              Niger and Methods of Use
     10 <130> FILE REFERENCE: UF-314XC1
     12 <140> CURRENT APPLICATION NUMBER: US 10/644,123A
     13 <141> CURRENT FILING DATE: 2003-08-20
     15 <150> PRIOR APPLICATION NUMBER: US 60/404,892
     16 <151> PRIOR FILING DATE: 2002-08-20
     18 <160> NUMBER OF SEQ ID NOS: 10
     20 <170> SOFTWARE: PatentIn version 3.2
     22 <210> SEQ ID NO: 1
     23 <211> LENGTH: 1397
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     25 <213> ORGANISM: Aspergillus niger
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     30 atteacece gateategeg acceptatega teacaaggtg gatgegateg gggaaggeea
                                                                              180
     32 tgagcccttg ccctggcgca tgggagatgg agccaccatc atgggacccc gcaacaagga
     34 ccgtgagcgc cagaaccccg acatgctccg tcctccgagc accgaccatg gcaacatgcc
                                                                              240
                                                                              300
     36 qaacatgegg tggagetttg etgaeteeca cattegeatt gaggtaagee ettegagagt
                                                                              360
     38 cttgtgtacg acaagcaaaa taggctaatg cactgcagga gggcggctgg acacgccaga
                                                                              420
     40 ctaccqtacg cgagctgcca acaagcaggg agcttgctgg agtaaacatg cgccttgatg
     42 agggtgtcat tcgcgagctg cactggcatc gggaagcaga gtgggcgtat gtgctggccg
                                                                              480
     44 qacqtqtacq aqtgactggt cttgacctgg agggaggcag cttcatcgat gacctggaag
                                                                              540
     46 agggtgacct ctggtacttc ccatcgggcc atccccattc acttcagggt ctcagtccta
                                                                              600
     48 atggcaccga gttcttactg atcttcgacg atggaaactt ttccgaggag tcaacgttct
                                                                              660
     50 tgttgaccga ctggatcggt atgtccatca ctatgctgtt gtacaacctc cacaaaaata
                                                                              720
     52 ctaacaatgc tataaaacag cacatacacc caagtctgtc ctcgccggaa acttccgcat
                                                                              780
                                                                              840
     54 gegeceacaa acatteaaga acateecace atetgaaaag tacatettee agggetetgt
                                                                              900
     56 cccaqactct atccccaaag aacttccccg caacttcaaa gcatccaagc agcgcttcac
                                                                              960
     58 gcataagatg ctcgctcaag aacccgagca tacctctggc ggagaggtgc gcatcacaga
                                                                             1020
     60 ctcgtccaac tttcccatct ccaagacggt cgcggccgcc cacctgacca ttaacccggg
                                                                             1080
     62 cgctatccgg gagatgcact ggcatcccaa tgcggatgaa tggtcctact ttaagcgcgg
     64 tcgggcgcga gtgactatct tcgctgctga aggtaatgct cgtacattcg actacgtagc
                                                                             1140
     66 qqqaqatqtq qqcattqttc ctcqcaacat qqqtcatttc attgagaacc tcagtgatga
                                                                             1200
                                                                             1260
     68 cqaqqaqqtc qaqqtqttqq aaatcttccq qqcgqaccqa ttccgggact tttcgttgtt
                                                                             1320
     70 ccagtggatg ggagagacgc cgcagcggat ggtggcagag catgtgttta aggatgatcc
                                                                             1380
     72 agatqcqqcc agggagttcc ttaagagtgt ggagagcggg gagaaggatc caattcggag
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     74 cccaaqtqaq taqatqa
     77 <210> SEO ID NO: 2
     78 <211> LENGTH: 1280
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Input Set : D:\UF-314XC1.txt

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80 <213 > ORGANISM: Aspergillus niger
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85 attcacccc gatcatcgcg acccctatga tcacaaggtg gatgcgatcg gggaaggcca
                                                                          120
                                                                          180
87 tgagcccttg ccctggcgca tgggagatgg agccaccatc atgggacccc gcaacaagga
89 cegtgagege cagaaceceg acatgeteeg tecteegage acegaceatg geaacatgee
                                                                          240
91 gaacatgegg tggagetttg etgaeteeca cattegeatt gaggagggeg getggaeaeg
                                                                          300
93 ccagactacc gtacgcgagc tgccaacaag caaggagctt gctggagtaa acatgcgcct
                                                                          360
95 tqatqaqqqt gtcattcqcq aqctgcactq qcatcgqgaa gcagaqtggg cgtatgtgct
                                                                          420
97 ggccggacgt gtacgagtga ctggtcttga cctggaggga ggcagcttca tcgatgacct
                                                                          480
99 qqaaqaqqqt qacctctqqt acttcccatc ggqccatccc cattcacttc agggtctcag
                                                                          540
                                                                           600
101 tectaatqqc accqaqttet tactqatett egacgatgga aaetttteeg aggagteaae
103 qttcttqttq accqactqqa tcqcacatac acccaagtct gtcctcgccg gaaacttccg
                                                                           660
105 catgegeeca caaacattea agaacateec accatetgaa aagtacatet teeagggete
                                                                           720
                                                                           780
107 tqtcccaqac tctatcccca aaqaacttcc ccgcaacttc aaagcatcca agcagcgctt
109 cacqcataaq atqctcqctc aagaacccqa gcatacctct ggcggagagg tgcgcatcac
                                                                           840
111 agactegtee aacttteeca tetecaagae ggtegeggee geecacetga ceattaacee
                                                                           900
113 gggcgctatc cgggagatgc actggcatcc caatgcggat gaatggtcct actttaagcg
                                                                           960
                                                                          1020
115 cggtcgggcg cgagtgacta tcttcgctgc tgaaggtaat gctcgtacat tcgactacgt
117 agegggagat gtgggcattg tteetegeaa catgggteat tteattgaga aceteagtga
                                                                          1080
119 tgacgaggag gtcgaggtgt tggaaatctt ccgggcggac cgattccggg acttttcgtt
                                                                          1140
121 gttccagtgg atgggagaga cgccgcagcg gatggtggca gagcatgtgt ttaaggatga
                                                                          1200
123 tocagatgcg gccagggagt toottaagag tgtggagagc ggggagaagg atccgattcg
                                                                          1260
                                                                          1280
125 gagcccaagt gagtagatga
128 <210> SEQ ID NO: 3
129 <211> LENGTH: 424
130 <212> TYPE: PRT
131 <213> ORGANISM: Aspergillus niger
133 <400> SEQUENCE: 3
135 Tyr Gln Gln Leu Leu Gln Ile Pro Ala Ser Ser Pro Ser Ile Phe Phe
136 1
                    5
                                         10
139 Gln Asp Lys Pro Phe Thr Pro Asp His Arq Asp Pro Tyr Asp His Lys
140
                20
                                     25
143 Val Asp Ala Ile Gly Glu Gly His Glu Pro Leu Pro Trp Arg Met Gly
                                 40
.147 Asp Gly Ala Thr Ile Met Gly Pro Arg Asn Lys Asp Arg Glu Arg Gln
                             55
151 Asn Pro Asp Met Leu Arg Pro Pro Ser Thr Asp His Gly Asn Met Pro
152 65
                         70
155 Asn Met Arg Trp Ser Phe Ala Asp Ser His Ile Arg Ile Glu Glu Gly
156
                    85
                                         90
159 Gly Trp Thr Arg Gln Thr Thr Val Arg Glu Leu Pro Thr Ser Arg Glu
                100
                                     105
163 Leu Ala Gly Val Asn Met Arg Leu Asp Glu Gly Val Ile Arg Glu Leu
                                                     125
164
            115
                                 120
167, His Trp His Arg Glu Ala Glu Trp Ala Tyr Val Leu Ala Gly Arg Val
                             135
171 Arg Val Thr Gly Leu Asp Leu Glu Gly Gly Ser Phe Ile Asp Asp Leu
```

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Input Set : D:\UF-314XC1.txt

172	145					150					155					160
		Glu	Gly	Asp	Leu	Trp	Tyr	Phe	Pro	Ser	Gly	His	Pro	His	Ser	Leu
176			_	_	165	_	_			170	_				175	
179	Gln	Gly	Leu	Ser	Pro	Asn	Gly	Thr	Glu	Phe	Leu	Leu	Ile	Phe	Asp	Asp
180				180					185					190		
183	Gly	Asn	Phe	Ser	Glu	Glu	Ser	Thr	Phe	Leu	Leu	Thr	Asp	Trp	Ile	Ala
184			195					200					205			
187	His	Thr	Pro	Lys	Ser	Val	Leu	Ala	Gly	Asn	Phe	Arg	Met	Arg	Pro	Gln
188		210					215					220				
191	Thr	Phe	Lys	Asn	Ile	Pro	Pro	Ser	Glu	Lys		Ile	Phe	Gln	Gly	Ser
	225				_	230		_			235		_			240
	Val	Pro	Asp	Ser		Pro	Lys	Glu	Leu		Arg	Asn	Phe	Lys		Ser
196		-			245		_		_	250	-		_		255	_,
	Lys	GIn	Arg		Thr	Hıs	Lys	Met	Leu	Ala	GIn	GIu	Pro		His	Thr
200		~ 7	~ 1	260			-1	m)	265		a	3	D1	270	T 3 -	0
	Ser	GIY	_	GIU	vaı	Arg	тте		Asp	Ser	Ser	Asn		Pro	шe	ser
204	T	mb ~	275	- ות	77.	77.	II i a	280	The	710	7 an	Dro	285	777	Tlo	7 ~~
207	цуѕ	290	Val	Ala	Ala	Ala	295	Leu	Thr	TIE	ASII	300	GIY	AIA	ire	Arg
	Glu		ніс	Trn	Hic	Dro		7. l =	Asp	Glu	Trn		Tur	Dhe	Luc	Δra
	305	Mec	1112	ırp	1113	310	ASII	ΑΙα	Аэр	GIU	315	DCI	TYT	LIIC	цуз	320
		Ara	Ala	Ara	Val		Tle	Phe	Ala	Ala		ĠĮv	Asn	Ala	Ara	
216	017			3	325					330	0_0	0-1			335	
	Phe	Asp	Tvr	Val		Glv	Asp	Val	Gly		Val	Pro	Arq	Asn		Gly
220		_	2	340		2	r		345					350		*
223	His	Phe	Ile	Glu	Asn	Leu	Ser	Asp	Asp	Glu	Glu	Val	Glu	Val	Leu	Glu
224			355					360					365			
227	Ile	Phe	Arg	Ala	Asp	Arg	Phe	Arg	Asp	Phe	Ser	Leu	Phe	Gln	Trp	Met
228		370					375					380				
231	Gly	Glu	Thr	Pro	Gln	Arg	Met	Val	Ala	Glu	His	Val	Phe	Lys	Asp	Asp
	385					390					395					400
	Pro	Asp	Ala	Ala	-	Glu	Phe	Leu	Lys		Val	Glu	Ser	Gly		Lys
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			_													
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		<212> TYPE: PRT <213> ORGANISM: Aspergillus niger														
	<400> SEQUENCE:							mger								
						Dhe	Thr	Pro	Asp	нiс	Ara	Asn	Pro	Tvr	Asn	His
251		GIII	MSP	шуз	5	rne	1111	110	Asp	10	Arg	изр	110	T Y L	15	111.5
		Val	Asp	Ala	_	Glv	Glu	Glv	His		Pro	Len	Pro	Trp		Met
255	-1-		p	20		 1	0_0	0-1	25					30	5	
	Glv	Asp	Glv		Thr	Ile	Met	Glv	Pro	Ara	Asn	Lys	Asp		Glu	Arq
259	-	1	35					40	_	,		4	45	J		
262	Gln	Asn	Pro	Asp	Met	Leu	Arg	Pro	Pro	Ser	Thr	Asp	His	Gly	Asn	Met
263		50		-			55					60		-		
266	Pro	Asn	Met	Arg	Trp	Ser	Phe	Ala	Asp	Ser	His	Ile	Arg	Ile	Glu	Glu

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```
267 65
270 Gly Gly Trp Thr Arg Gln Thr Thr Val Arg Glu Leu Pro Thr Ser Arg
274 Glu Leu Ala Gly Val Asn Met Arg Leu Asp Glu Gly Val Ile Arg Glu
               100
                                   105
278 Leu His Trp His Arg Glu Ala Glu Trp Ala Tyr Val Leu Ala Gly Arg
                               120
282 Val Arg Val Thr Gly Leu Asp Leu Glu Gly Gly Ser Phe Ile Asp Asp
                           135
                                               140
286 Leu Glu Glu Gly Asp Leu Trp Tyr Phe Pro Ser Gly His Pro His Ser
                       150
                                           155
290 Leu Gln Gly Leu Ser Pro Asn Gly Thr Glu Phe Leu Leu Ile Phe Asp
                   165
                                       170
294 Asp Gly Asn Phe Ser Glu Glu Ser Thr Phe Leu Leu Thr Asp Trp Ile
               1.80
                                   185
298 Ala His Thr Pro Lys Ser Val Leu Ala Gly Asn Phe Arg Met Arg Pro
           195
                                200
                                                    205
302 Gln Thr Phe Lys Asn Ile Pro Pro Ser Glu Lys Tyr Ile Phe Gln Gly
       210
                           215
                                               220
306 Ser Val Pro Asp Ser Ile Pro Lys Glu Leu Pro Arg Asn Phe Lys Ala
                       230
                                           235
310 Ser Lys Gln Arg Phe Thr His Lys Met Leu Ala Gln Glu Pro Glu His
                                       250
                   245
314 Thr Ser Gly Gly Glu Val Arg Ile Thr Asp Ser Ser Asn Phe Pro Ile
                                   265
318 Ser Lys Thr Val Ala Ala Ala His Leu Thr Ile Asn Pro Gly Ala Ile
319 275
                               280
                                                   285
322 Arg Glu Met His Trp His Pro Asn Ala Asp Glu Trp Ser Tyr Phe Lys
                           295
326 Arg Gly Arg Ala Arg Val Thr Ile Phe Ala Ala Glu Gly Asn Ala Arg
                       310
                                           315
330 Thr Phe Asp Tyr Val Ala Gly Asp Val Gly Ile Val Pro Arg Asn Met
                   325
                                       330
334 Gly His Phe Ile Glu Asn Leu Ser Asp Asp Glu Glu Val Glu Val Leu
               340
                                   345
338 Glu Ile Phe Arg Ala Asp Arg Phe Arg Asp Phe Ser Leu Phe Gln Trp
          355
                               360
342 Met Gly Glu Thr Pro Gln Arg Met Val Ala Glu His Val Phe Lys Asp
343 370
                          375
346 Asp Pro Asp Ala Ala Arg Glu Phe Leu Lys Ser Val Glu Ser Gly Glu
347 385
                       390
                                           395
350 Lys Asp Pro Ile Arg Ser Pro Ser Glu
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354 <210> SEQ ID NO: 5
355 <211> LENGTH: 21
356 <212> TYPE: DNA
357 <213> ORGANISM: Artificial sequence
359 <220> FEATURE:
360 <223> OTHER INFORMATION: PCR primer
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Input Set : D:\UF-314XC1.txt

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362 <400> SEQUENCE: 5
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363 gtcctcgaga aaagatacca g
366 <210> SEQ ID NO: 6
367 <211> LENGTH: 27
368 <212> TYPE: DNA
369 <213> ORGANISM: Artificial sequence
371 <220> FEATURE:
372 <223> OTHER INFORMATION: PCR primer
374 <400> SEQUENCE: 6
375 tcatctactc acttgggctc cgaattg
                                                                          27
378 <210> SEQ ID NO: 7
379 <211> LENGTH: 11
380 <212> TYPE: PRT
381 <213> ORGANISM: Aspergillus niger
383 <400> SEQUENCE: 7
385 Phe Gln Asp Lys Pro Phe Thr Pro Asp His Arg
386 1
389 <210> SEQ ID NO: 8
390 <211> LENGTH: 4
391 <212> TYPE: PRT
392 <213> ORGANISM: Artificial sequence
394 <220> FEATURE:
395 <223> OTHER INFORMATION: Anticipated N-terminal sequence of oxalate decarboxylase of
        Aspergillus niger
398 <400> SEQUENCE: 8
400 Tyr Gln Gln Asp
401 1
404 <210> SEQ ID NO: 9
405 <211> LENGTH: 385
406 <212> TYPE: PRT
407 <213> ORGANISM: Bacillus subtilis
409 <400> SEQUENCE: 9
411 Met Lys Lys Gln Asn Asp Ile Pro Gln Pro Ile Arg Gly Asp Lys Gly
412 1
415 Ala Thr Val Lys Ile Pro Arg Asn Ile Glu Arg Asp Arg Gln Asn Pro
419 Asp Met Leu Val Pro Pro Glu Thr Asp His Gly Thr Val Ser Asn Met
420 35
                                40
423 Lys Phe Ser Phe Ser Asp Thr His Asn Arg Leu Glu Lys Gly Gly Tyr
                            55
427 Ala Arg Glu Val Thr Val Arg Glu Leu Pro Ile Ser Glu Asn Leu Ala
                        70
                                            75
431 Ser Val Asn Met Arg Leu Lys Pro Gly Ala Ile Arg Glu Leu His Trp
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435 His Lys Glu Ala Glu Trp Ala Tyr Met Ile Tyr Gly Ser Ala Arg Val
436
439 Thr Ile Val Asp Glu Lys Gly Arg Ser Phe Ile Asp Asp Val Gly Glu
                                120
           115
443 Gly Asp Leu Trp Tyr Phe Pro Ser Gly Leu Pro His Ser Ile Gln Ala
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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/644,123A

DATE: 02/04/2005 TIME: 07:26:31

Input Set : D:\UF-314XC1.txt